

Elena N Ilina

List of Publications by Year in Descending Order

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Version: 2024-04-24

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

100
papers

1,825
citations

23
h-index

40
g-index

119
ext. papers

2,353
ext. citations

3.9
avg, IF

4.03
L-index

#	Paper	IF	Citations
100	Drift of the Subgingival Periodontal Microbiome during Chronic Periodontitis in Type 2 Diabetes Mellitus Patients. <i>Pathogens</i> , 2021 , 10,	4.5	3
99	Separation of Donor and Recipient Microbial Diversity Allows Determination of Taxonomic and Functional Features of Gut Microbiota Restructuring following Fecal Transplantation. <i>MSystems</i> , 2021 , 6, e0081121	7.6	0
98	Novel K23-Specific Bacteriophages From Different Families: Similarity of Depolymerases and Their Therapeutic Potential. <i>Frontiers in Microbiology</i> , 2021 , 12, 669618	5.7	4
97	Molecular genetic characterization of three new Klebsiella pneumoniae bacteriophages suitable for phage therapy 2021 ,		1
96	The effects of <i>Levilactobacillus brevis</i> on the physiological parameters and gut microbiota composition of rats subjected to desynchronization.. <i>Microbial Cell Factories</i> , 2021 , 20, 226	6.4	0
95	Metabolic Changes of during the Anti-Tuberculosis Therapy. <i>Pathogens</i> , 2020 , 9,	4.5	6
94	Gut microbiota assessment in Moscow long-livers using next generation sequencing. <i>Bulletin of Russian State Medical University</i> , 2020 , 16-20	0.4	
93	Evaluation of the Levels of Metabolites in Feces of Patients with Inflammatory Bowel Diseases. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2020 , 14, 312-319	0.4	1
92	Efficacy of commercial bacteriophage products against ESKAPE pathogens 2020 , 18-24	0.2	5
91	Identification of Clinically Significant Prostate Cancer by Combined and mRNA Detection in Urine Samples. <i>Research and Reports in Urology</i> , 2020 , 12, 403-413	1.3	3
90	Genome Complexity Browser: Visualization and quantification of genome variability. <i>PLoS Computational Biology</i> , 2020 , 16, e1008222	5	1
89	Transcriptional Landscape of Bacteriophage vB_SauM-515A1. <i>Viruses</i> , 2020 , 12,	6.2	4
88	Gene Networks Underlying the Resistance of to Inflammatory Factors. <i>Frontiers in Immunology</i> , 2020 , 11, 595877	8.4	2
87	Aureolic Acid Group of Agents as Potential Antituberculosis Drugs. <i>Antibiotics</i> , 2020 , 9,	4.9	1
86	Contribution of Podoviridae and Myoviridae bacteriophages to the effectiveness of anti-staphylococcal therapeutic cocktails. <i>Scientific Reports</i> , 2020 , 10, 18612	4.9	10
85	Phigaro: high-throughput prophage sequence annotation. <i>Bioinformatics</i> , 2020 , 36, 3882-3884	7.2	23
84	Deep Functional Profiling Facilitates the Evaluation of the Antibacterial Potential of the Antibiotic Amicoumacin. <i>Antibiotics</i> , 2020 , 9,	4.9	6

83	Genome Complexity Browser: Visualization and quantification of genome variability 2020 , 16, e1008222		
82	Genome Complexity Browser: Visualization and quantification of genome variability 2020 , 16, e1008222		
81	Genome Complexity Browser: Visualization and quantification of genome variability 2020 , 16, e1008222		
80	Genome Complexity Browser: Visualization and quantification of genome variability 2020 , 16, e1008222		
79	VERA: agent-based modeling transmission of antibiotic resistance between human pathogens and gut microbiota. <i>Bioinformatics</i> , 2019 , 35, 3803-3811	7.2	3
78	Proteogenomic analysis of Mycobacterium tuberculosis Beijing B0/W148 cluster strains. <i>Journal of Proteomics</i> , 2019 , 192, 18-26	3.9	8
77	Shifts in the Human Gut Microbiota Structure Caused by Quadruple Eradication Therapy. <i>Frontiers in Microbiology</i> , 2019 , 10, 1902	5.7	17
76	The role of IS6110 in micro- and macroevolution of Mycobacterium tuberculosis lineage 2. <i>Molecular Phylogenetics and Evolution</i> , 2019 , 139, 106559	4.1	6
75	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019 , 4, 1727-1736	26.6	100
74	Faecal Transplant in GIT Treatment (Pilot Clinical Experience). <i>Doctor Ru</i> , 2019 , 158, 40-46	1.3	4
73	Comparative genomics of the Escherichia coli strains AB1157, AB2463, AB2494 and AB1885. <i>Molekuliarnaia Genetika, Mikrobiologiya I Virusologiya</i> , 2019 , 37, 134	0.3	
72	System OMICs analysis of Mycobacterium tuberculosis Beijing B0/W148 cluster. <i>Scientific Reports</i> , 2019 , 9, 19255	4.9	7
71	Long-term impact of fecal transplantation in healthy volunteers. <i>BMC Microbiology</i> , 2019 , 19, 312	4.5	24
70	The Influence of Cultivation Conditions on the Proteomic Profile of Mycobacterium tuberculosis H37Rv. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2018 , 12, 32-38	0.4	
69	Draft genomes of strains isolated from human feces before and after eradication therapy against. <i>Data in Brief</i> , 2018 , 16, 511-514	1.2	2
68	M. BOVIS BCG-1 (RUSSIA) SUB-STRAIN GENOME STABILITY INVESTIGATION WITHIN THE ENTIRE PRODUCTION PROCESS. <i>Zhurnal Mikrobiologii Epidemiologii I Immunobiologii</i> , 2018 , 58-67	0.5	2
67	Mutants resistant to nalidixic acid and novobiocin. specific features of formation from E. Coli strains with RecA or LexA mutations. <i>Molekuliarnaia Genetika, Mikrobiologiya I Virusologiya</i> , 2018 , 36, 26	0.3	
66	Characteristics of Emergence of Mutants Resistant to Nalidixic Acid and Novobiocin in E. coli Strains with recA and lexA Mutations. <i>Molecular Genetics, Microbiology and Virology</i> , 2018 , 33, 30-33	0.4	3

65	Ultrahigh-throughput functional profiling of microbiota communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 9551-9556	11.5	43
64	Data on gut metagenomes of the patients with infection before and after the antibiotic therapy. <i>Data in Brief</i> , 2017 , 11, 68-71	1.2	9
63	Data on gut metagenomes of the patients with alcoholic dependence syndrome and alcoholic liver cirrhosis. <i>Data in Brief</i> , 2017 , 11, 98-102	1.2	5
62	Microfluidic droplet platform for ultrahigh-throughput single-cell screening of biodiversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 2550-2555	11.5	124
61	Genetic Environment of the blaKPC-2 Gene in a Klebsiella pneumoniae Isolate That May Have Been Imported to Russia from Southeast Asia. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	5
60	Metagenomic Analysis of Gingival Sulcus Microbiota and Pathogenesis of Periodontitis Associated with Type 2 Diabetes Mellitus. <i>Bulletin of Experimental Biology and Medicine</i> , 2017 , 163, 718-721	0.8	13
59	Links of gut microbiota composition with alcohol dependence syndrome and alcoholic liver disease. <i>Microbiome</i> , 2017 , 5, 141	16.6	158
58	Inhibitory effect of streptococci on the growth of M. catarrhalis strains and the diversity of putative bacteriocin-like gene loci in the genomes of S. pneumoniae and its relatives. <i>AMB Express</i> , 2017 , 7, 218	4.1	1
57	Evolutionary pathway analysis and unified classification of East Asian lineage of Mycobacterium tuberculosis. <i>Scientific Reports</i> , 2017 , 7, 9227	4.9	64
56	Genome analysis of E. coli isolated from Crohn's disease patients. <i>BMC Genomics</i> , 2017 , 18, 544	4.5	15
55	FEATURES OF ESCHERICHIA COLI CLINICAL STRAINS, ISOLATED FROM THE PATIENTS WITH CROHN'S DISEASE. <i>Zhurnal Mikrobiologii Epidemiologii I Immunobiologii</i> , 2017 , 42-49	0.5	
54	State of the Art of Chromosome 18-Centric HPP in 2016: Transcriptome and Proteome Profiling of Liver Tissue and HepG2 Cells. <i>Journal of Proteome Research</i> , 2016 , 15, 4030-4038	5.6	16
53	Large scale analysis of amino acid substitutions in bacterial proteomics. <i>BMC Bioinformatics</i> , 2016 , 17, 450	3.6	2
52	The mystery of the fourth clone: comparative genomic analysis of four non-typeable Streptococcus pneumoniae strains with different susceptibilities to optochin. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016 , 35, 119-30	5.3	4
51	Analysis of nosocomial Staphylococcus haemolyticus by MLST and MALDI-TOF mass spectrometry. <i>Infection, Genetics and Evolution</i> , 2016 , 39, 99-105	4.5	11
50	The ability of various strains of Staphylococcus to create biofilms and their effect on cells of the human body. <i>Molecular Genetics, Microbiology and Virology</i> , 2016 , 31, 21-29	0.4	
49	Metagenomic analysis of taxonomic and functional changes in gut microbiota of patients with the alcohol dependence syndrome. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2016 , 10, 184-190	0.4	
48	Proteome analysis of the Mycobacterium tuberculosis Beijing B0/W148 cluster. <i>Scientific Reports</i> , 2016 , 6, 28985	4.9	16

47	Complete Genome Sequence of Mycobacterium bovis Strain BCG-1 (Russia). <i>Genome Announcements</i> , 2016 , 4,		11
46	Variability in the relative human DNA content during metagenomic analysis of gut microbiota. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2015 , 9, 290-295	0.4	
45	Molecular mechanisms of formation of drug resistance in Neisseria gonorrhoeae: History and prospects. <i>Molecular Genetics, Microbiology and Virology</i> , 2015 , 30, 132-140	0.4	4
44	Species Diversity of Bifidobacteria in the Intestinal Microbiota Studied Using MALDI-TOF Mass-Spectrometry. <i>Vestnik Rossiiskoi Akademii Meditsinskikh Nauk</i> , 2015 , 70, 435-440	0.4	11
43	Chromosome 18 transcriptoproteome of liver tissue and HepG2 cells and targeted proteome mapping in depleted plasma: update 2013. <i>Journal of Proteome Research</i> , 2014 , 13, 183-90	5.6	33
42	Emergence of carbapenemase-producing Gram-negative bacteria in Saint Petersburg, Russia. <i>International Journal of Antimicrobial Agents</i> , 2014 , 44, 152-5	14.3	44
41	Long-term dissemination of CTX-M-5-producing hypermutable Salmonella enterica serovar typhimurium sequence type 328 strains in Russia, Belarus, and Kazakhstan. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 5202-10	5.9	9
40	Analysis of the genetic determinants of multidrug and extensive drug resistance in Mycobacterium tuberculosis with the use of an oligonucleotide microchip. <i>Molecular Biology</i> , 2014 , 48, 214-226	1.2	3
39	Genome-wide Mycobacterium tuberculosis variation (GMTV) database: a new tool for integrating sequence variations and epidemiology. <i>BMC Genomics</i> , 2014 , 15, 308	4.5	61
38	Spoligotyping of Mycobacterium tuberculosis complex isolates using hydrogel oligonucleotide microarrays. <i>Infection, Genetics and Evolution</i> , 2014 , 26, 41-6	4.5	17
37	RNA-Seq gene expression profiling of HepG2 cells: the influence of experimental factors and comparison with liver tissue. <i>BMC Genomics</i> , 2014 , 15, 1108	4.5	28
36	Unusual large-scale chromosomal rearrangements in Mycobacterium tuberculosis Beijing B0/W148 cluster isolates. <i>PLoS ONE</i> , 2014 , 9, e84971	3.7	15
35	Strain differentiation of Staphylococcus aureus by means of direct MALDI TOF mass spectrometry profiling. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2013 , 7, 70-78	0.4	1
34	Discrimination between Streptococcus pneumoniae and Streptococcus mitis based on sorting of their MALDI mass spectra. <i>Clinical Microbiology and Infection</i> , 2013 , 19, 1066-71	9.5	55
33	Chromosome 18 transcriptome profiling and targeted proteome mapping in depleted plasma, liver tissue and HepG2 cells. <i>Journal of Proteome Research</i> , 2013 , 12, 123-34	5.6	46
32	Multiple-locus variable number tandem repeat analysis of Neisseria gonorrhoeae isolates in Russia. <i>Infection, Genetics and Evolution</i> , 2013 , 14, 8-14	4.5	2
31	Comparative genomic analysis of Mycobacterium tuberculosis drug resistant strains from Russia. <i>PLoS ONE</i> , 2013 , 8, e56577	3.7	37
30	Mutation in ribosomal protein S5 leads to spectinomycin resistance in Neisseria gonorrhoeae. <i>Frontiers in Microbiology</i> , 2013 , 4, 186	5.7	32

29	Mass spectrometry based methods for the discrimination and typing of mycobacteria. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 838-45	4.5	36
28	First detection of VIM-4 metallo-β-lactamase-producing Escherichia coli in Russia. <i>Clinical Microbiology and Infection</i> , 2012 , 18, E214-7	9.5	19
27	Application of MALDI-TOF mass spectrometry for differentiation of closely related species of the <i>Arthrobacter crystallopoietes</i> phylogenetic group. <i>Microbiology</i> , 2012 , 81, 696-701	1.4	6
26	Misidentification of alpha-hemolytic streptococci by routine tests in clinical practice. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 1709-15	4.5	41
25	Molecular typing of Mycobacterium tuberculosis circulated in Moscow, Russian Federation. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2011 , 30, 181-91	5.3	17
24	Comparative evaluation of new typing schemes for urogenital Chlamydia trachomatis isolates. <i>FEMS Immunology and Medical Microbiology</i> , 2010 , 59, 188-96		22
23	Molecular surveillance of clinical Neisseria gonorrhoeae isolates in Russia. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 3681-9	9.7	17
22	Molecular genetic characterization of methicillin-resistant Staphylococcus aureus isolates recovered from Moscow clinics. <i>Molecular Genetics, Microbiology and Virology</i> , 2010 , 25, 66-70	0.4	2
21	Mass-spectrometry analysis of genetic markers of S. pneumoniae resistance to β-lactam antibiotics. <i>Molecular Genetics, Microbiology and Virology</i> , 2010 , 25, 106-117	0.4	
20	Application of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for the study of Helicobacter pylori. <i>Rapid Communications in Mass Spectrometry</i> , 2010 , 24, 328-34	2.2	35
19	High interlaboratory reproducibility of matrix-assisted laser desorption ionization-time of flight mass spectrometry-based species identification of nonfermenting bacteria. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 3732-4	9.7	150
18	Hepatitis B virus genetic typing using mass-spectrometry. <i>Bulletin of Experimental Biology and Medicine</i> , 2009 , 147, 220-5	0.8	7
17	Mass spectrometry of nucleic acids in molecular medicine. <i>Russian Journal of Bioorganic Chemistry</i> , 2009 , 35, 135-149	1	1
16	Direct bacterial profiling by matrix-assisted laser desorption-ionization time-of-flight mass spectrometry for identification of pathogenic Neisseria. <i>Journal of Molecular Diagnostics</i> , 2009 , 11, 75-86 ^{5.1}		86
15	A MALDI TOF MS-based minisequencing method for rapid detection of TEM-type extended-spectrum beta-lactamases in clinical strains of Enterobacteriaceae. <i>Journal of Microbiological Methods</i> , 2008 , 75, 385-91	2.8	21
14	Mechanisms of macrolide resistance among Streptococcus pneumoniae isolates from Russia. <i>Antimicrobial Agents and Chemotherapy</i> , 2008 , 52, 2260-2	5.9	18
13	Relation between genetic markers of drug resistance and susceptibility profile of clinical Neisseria gonorrhoeae strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2008 , 52, 2175-82	5.9	25
12	Direct evaluation of drug resistance parameters in gonococcus. <i>Bulletin of Experimental Biology and Medicine</i> , 2007 , 144, 227-30	0.8	2

11	Analysis of the contribution of molecular mechanisms into formation of gonococcal resistance to tetracycline. <i>Bulletin of Experimental Biology and Medicine</i> , 2007 , 144, 432-7	0.8	6
10	Molecular characteristics of rifampicin- and isoniazid-resistant Mycobacterium tuberculosis isolates from the Russian Federation. <i>Journal of Antimicrobial Chemotherapy</i> , 2007 , 59, 1057-64	5.1	62
9	Mass-spectrometry based minisequencing method for the rapid detection of drug resistance in Mycobacterium tuberculosis. <i>Journal of Microbiological Methods</i> , 2007 , 70, 395-405	2.8	18
8	Analysis of genetic markers of N. gonorrhoeae resistance to beta-lactam antibiotics. <i>Bulletin of Experimental Biology and Medicine</i> , 2006 , 141, 610-5	0.8	5
7	Detection of Fluoroquinolone Resistance Single-Nucleotide Polymorphisms in Neisseria gonorrhoeae gyrA and parC Using MALDI-TOF Mass Spectrometry. <i>Molecular Biology</i> , 2005 , 39, 806-814	1.2	10
6	A2144G Is the Main Mutation in the 23S rRNA Gene of Helicobacter pylori Associated with Clarithromycin Resistance. <i>Russian Journal of Genetics</i> , 2005 , 41, 1095-1100	0.6	
5	Matrix-assisted laser desorption ionization-time of flight (mass spectrometry) for hepatitis C virus genotyping. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 2810-5	9.7	34
4	Fluoroquinolone-resistant Neisseria gonorrhoeae isolates from Russia: molecular mechanisms implicated. <i>Journal of Antimicrobial Chemotherapy</i> , 2004 , 53, 653-6	5.1	16
3	Molecular typing of N. gonorrhoeae strains prevalent in the Russian Federation. <i>Bulletin of Experimental Biology and Medicine</i> , 2003 , 136, 179-82	0.8	4
2	Shifts in the gut microbiota structure caused by Helicobacter pylori eradication therapy		1
1	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage		5